

REPLACEMENT SHEET

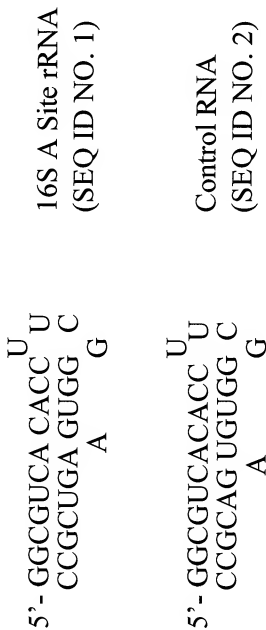


Figure 1. Sequence and structure of 27mer RNA target

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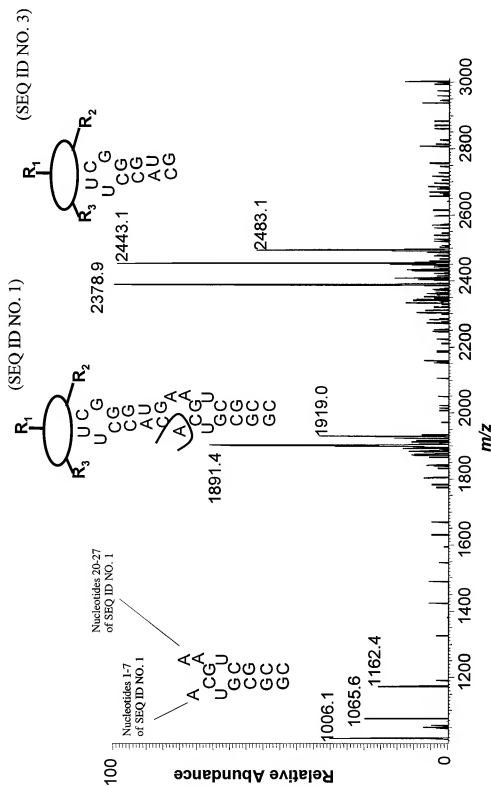


Figure 4. MS analysis of member bound to RNA/DNA chimera

The figure displays two mass spectra and a chemical structure. The left spectrum, labeled (SEQ ID NO. 1), shows the mass of RNA with a prominent peak at m/z 1784.4. The right spectrum, labeled (SEQ ID NO. 1), shows the mass of Paromomycin + RNA, with peaks at m/z 1907.5, 1919.8, 1929.4, 1952.9, and 1966.4. The chemical structure of a nucleoside is shown, consisting of a sugar ring with substituents R₁, R₂, and R₃, and a base (A, U, C, G).

RNA Spectrum (SEQ ID NO. 1):

m/z	Relative Abundance (%)
1784.4	100

Paromomycin + RNA Spectrum (SEQ ID NO. 1):

m/z	Relative Abundance (%)
1907.5	~15
1919.8	~10
1929.4	~10
1952.9	~10
1966.4	~10

Chemical Structure:

The structure shows a sugar ring with substituents R₁, R₂, and R₃, and a base (A, U, C, G). The base is attached to the sugar ring via a glycosidic bond.

Figure 5. ESI-MS of RNA/DNA chimera bound to paromomycin and library

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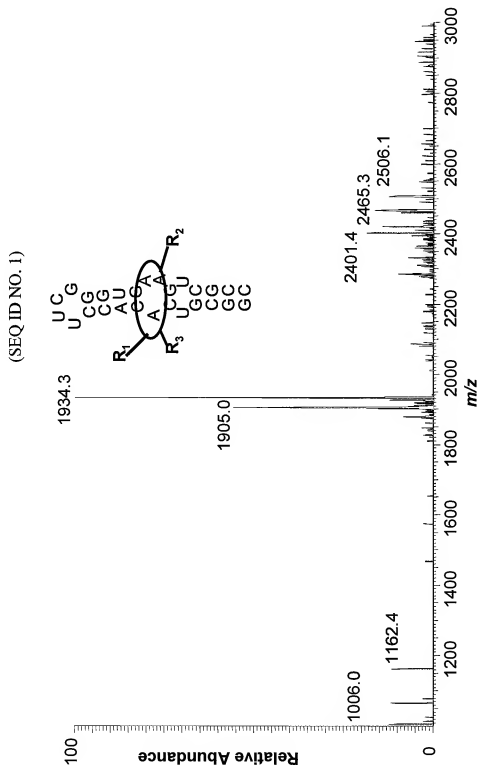


Figure 7. MS-MS analysis of member bound to RNA/DNA chimera at the A-Site

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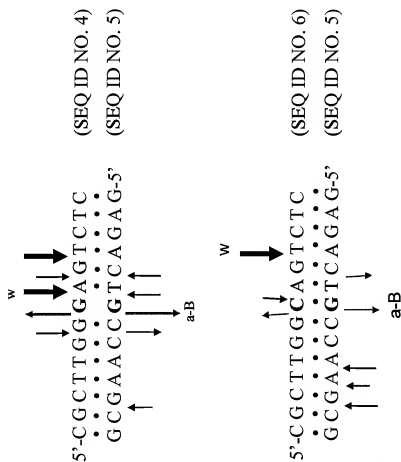


Figure 8. MS Fragmentation of DNA:DNA duplexes

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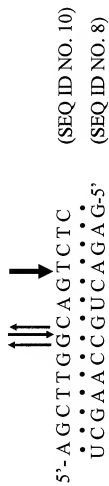
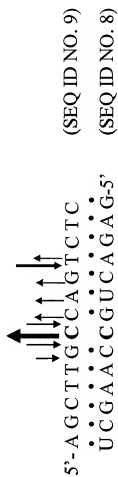
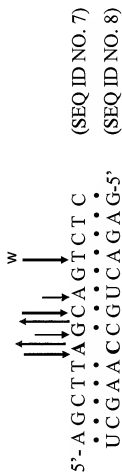


Figure 9. MS Fragmentation of DNA:RNA duplexes

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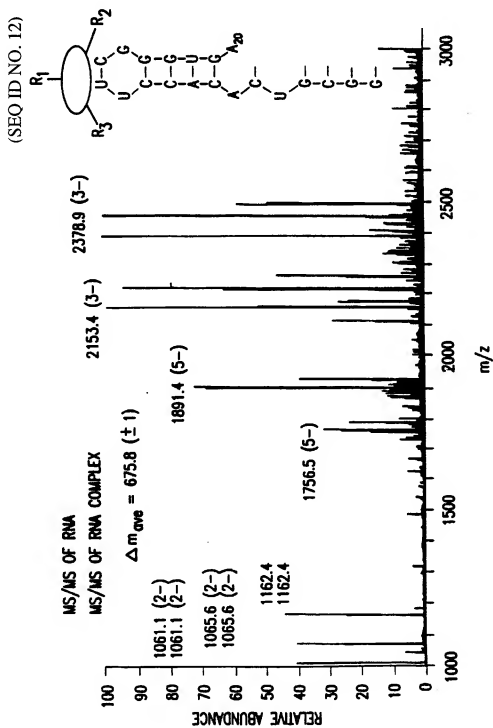


Figure 10

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(SEQ ID NO. 1)

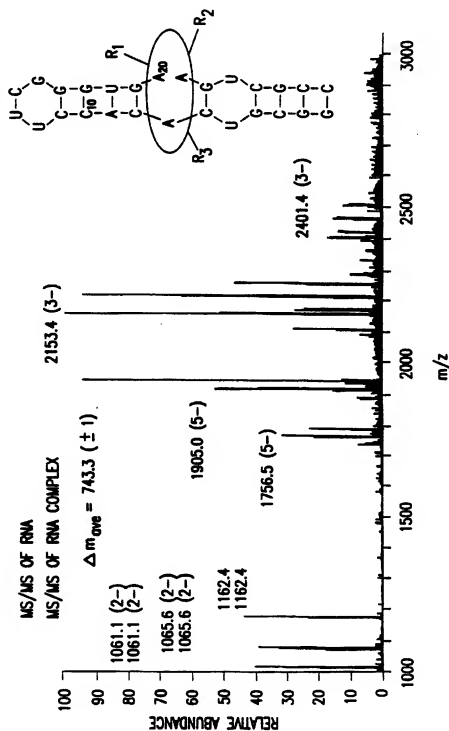


Figure 11

**MASS analysis of 16S A site RNA plus
216 member library**
(performed on quadrupole ion trap)

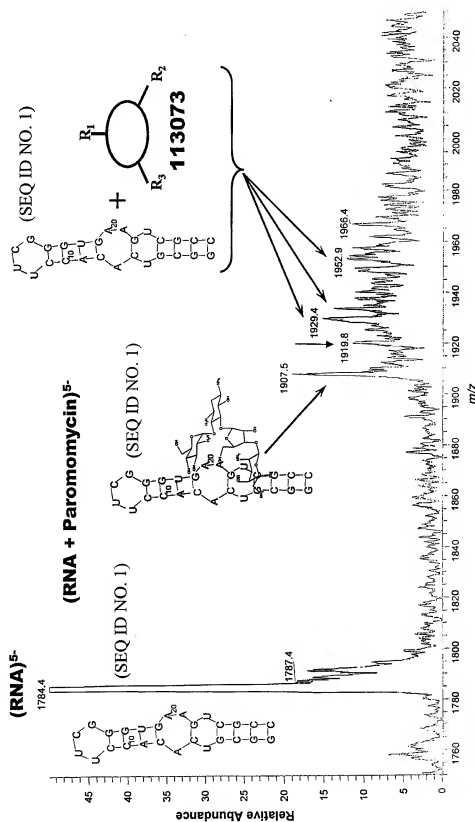
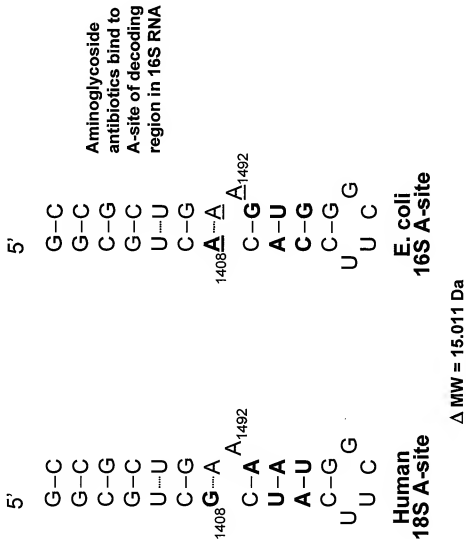


Figure 12

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(SEQ ID NO. 11)

(SEQ ID NO. 1)



Aminoglycoside
antibiotics bind to
A-site of decoding
region in 16S RNA

Figure 24. Eukaryotic and Prokaryotic A-Sites

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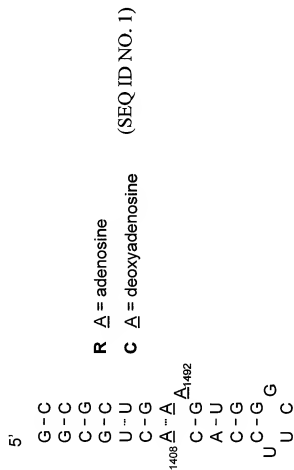


Figure 27